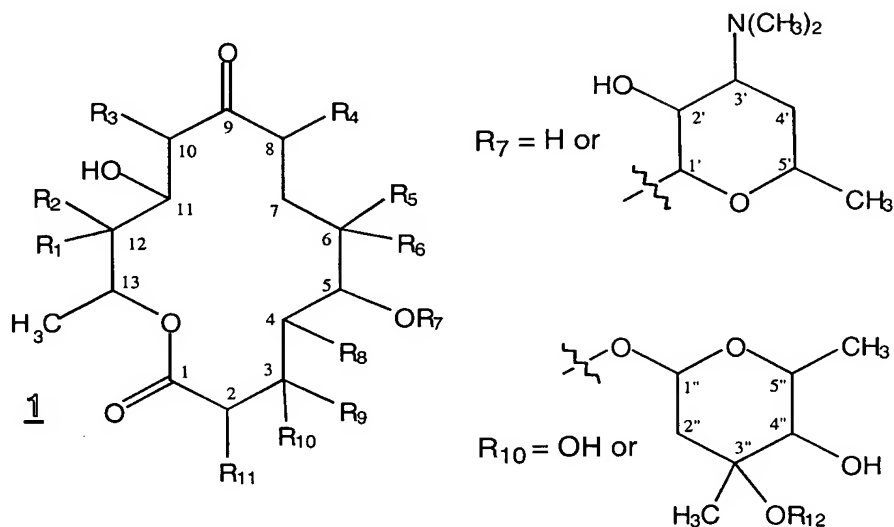


Claim Amendments:

1. – 25. (cancelled)

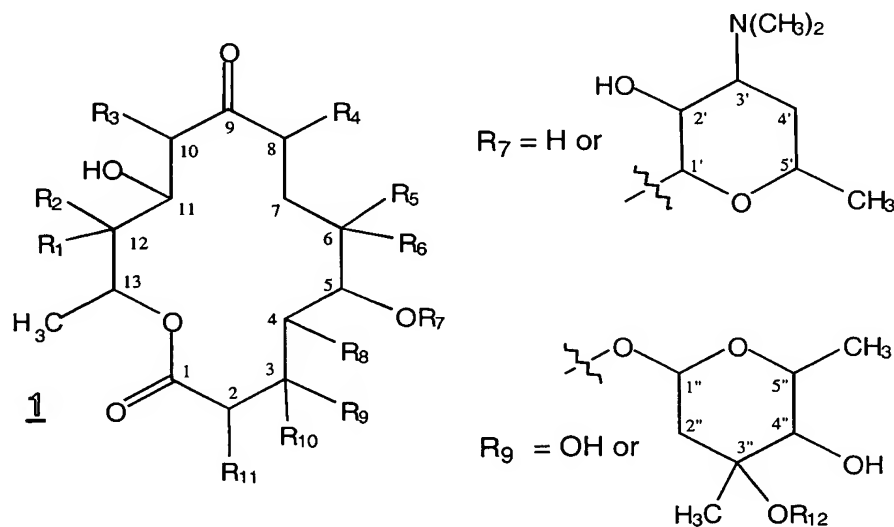
26. A process for making compounds of the formula 1:



wherein:

R₁ is H or OH; R₂-R₄ are each independently H, CH₃, or CH₂CH₃; R₅ is H or OH; and R₆ is H, CH₃, or CH₂CH₃; R₇ is H or desosamine; R₈ is H, CH₃, or CH₂CH₃; R₉ is OH, mycarose (R₁₂ is H), or cladinose (R₁₂ is CH₃), R₁₀ is H; or R₉ = R₁₀ = O; and R₁₁ is H, CH₃, or CH₂CH₃

27. A process for the production of compounds of formula 1



and to pharmaceutically acceptable salts thereof, wherein:

R₁ is H or OH; R₂-R₄ are each independently H, CH₃, or CH₂CH₃; R₅ is H or OH; and R₆ is H, CH₃, or CH₂CH₃; R₇ is H or desosamine; R₈ is H, CH₃, or CH₂CH₃; R₉ is OH, mycarose (R₁₂ is H), or cladinose (R₁₂ is CH₃), R₁₀ is H; or R₉ = R₁₀ = O; and R₁₁ is H, CH₃, or CH₂CH₃, with the proviso that when R₂-R₄ are CH₃, R₆ is CH₃, R₈ is CH₃, and R₁₁ is CH₃, then R₁ and R₅ are not H and R₁₂ is not H; or also when R₂-R₄ are CH₃, R₆ is CH₃, R₈ is CH₃, and R₁₁ is CH₃, then R₁ and R₅ are not OH and R₁₂ is not H; said process comprising culturing a transformant organism which contains a DNA gene assembly which produces a 14-membered macrolide, said gene assembly comprising a loading module of the form KSq-ATq-ACP where:

- a) KSq represents a domain operative to decarboxylate a malonate substrate carried by the ACP
- b) ATq represents an acyltransferase domain operative to load selectively a malonate unit onto the ACP; and
- c) ACP represents an acyl carrier protein

and a plurality of extension modules, wherein said extension modules are not usually associated with a loading module that effects decarboxylation of a malonyl residue.

28. The process of claim 27, wherein the loading module is selected from the oleandomycin, spiramycin, niddamycin, methymycin or monensin PKSs.

29. The process of claim 27, wherein the plurality of extension modules correspond to the extension modules of the erythromycin PKS.

30. The process of claim 28, wherein the plurality of extension modules correspond to the extension modules of the erythromycin PKS.

31. The process of claim 27, wherein the organism is selected from the group consisting of: *Saccharopolyspora erythraea*, *Streptomyces coelicolor*, *Streptomyces avermitilis*, *Streptomyces griseofuscus*, *Streptomyces cinnamonensis*, *Streptomyces fradiae*, *Streptomyces longisporoflavus*, *Streptomyces hygroscopicus*, *Micromonospora griseorubida*, *Streptomyces lasaliensis*, *Streptomyces venezuelae*, *Streptomyces antibioticus*, *Streptomyces lividans*, *Streptomyces rimosus*, *Streptomyces albus*, *Amycolatopsis mediterranei*, and *Streptomyces tsukubaensis*.

32. The process of claim 28, wherein the organism is selected from the group consisting of: *Saccharopolyspora erythraea*, *Streptomyces coelicolor*, *Streptomyces avermitilis*, *Streptomyces griseofuscus*, *Streptomyces cinnamonensis*, *Streptomyces fradiae*, *Streptomyces longisporoflavus*, *Streptomyces hygroscopicus*, *Micromonospora griseorubida*, *Streptomyces lasaliensis*, *Streptomyces venezuelae*, *Streptomyces antibioticus*, *Streptomyces lividans*, *Streptomyces rimosus*, *Streptomyces albus*, *Amycolatopsis mediterranei*, and *Streptomyces tsukubaensis*.

33. The process of claim 29, wherein the organism is selected from the group consisting of: *Saccharopolyspora erythraea*, *Streptomyces coelicolor*, *Streptomyces avermitilis*, *Streptomyces griseofuscus*, *Streptomyces cinnamonensis*, *Streptomyces fradiae*, *Streptomyces longisporoflavus*, *Streptomyces hygroscopicus*, *Micromonospora griseorubida*, *Streptomyces lasaliensis*, *Streptomyces venezuelae*, *Streptomyces antibioticus*, *Streptomyces lividans*, *Streptomyces rimosus*, *Streptomyces albus*, *Amycolatopsis mediterranei*, and *Streptomyces tsukubaensis*.

34. The process of claim 30, wherein the organism is selected from the group consisting of: *Saccharopolyspora erythraea*, *Streptomyces coelicolor*, *Streptomyces avermitilis*, *Streptomyces griseofuscus*, *Streptomyces cinnamonensis*, *Streptomyces fradiae*, *Streptomyces longisporoflavus*, *Streptomyces hygroscopicus*, *Micromonospora griseorubida*, *Streptomyces lasaliensis*, *Streptomyces venezuelae*, *Streptomyces antibioticus*, *Streptomyces lividans*, *Streptomyces rimosus*, *Streptomyces albus*, *Amycolatopsis mediterranei*, and *Streptomyces tsukubaensis*.

35. The process of claim 27, which additionally comprises recovering a compound of formula 1.